strains previously characterised in North America, but in a separate clade from strains of the subspecies *multiplex* previously sequenced in Europe, supporting the hyphothesis that they originate from a distinct introduction that occured in Europe. Pathogenicity tests on *Prunus* spp. and grapes are ongoing to assess the virulence and the host range of this newly discovered variant of *X. fastidiosa*.

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Identification of multilocus SSR markers to assess genetic diversity of *Xylella fastidiosa* subsp. *pauca*, ST53, spreading in Apulia (southern Italy)

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Abstract: The epidemic spread of *Xylella fastidiosa* in Apulia (southern Italy) with the continuous expansions of the border of the infected area, incited several investigations into the genetics and genomics of the strains associated with the infections. These studies were aimed to infer genetic correlations with known strains of the bacterium as well as among the initially discovered Apulian outbreaks and those that emerged from time to time. MLST and full genome sequencing provided clear evidence that a single genotype, denoted ST53, of the subspecies *pauca* was causing the epidemics on olives and other hosts. In this work, we tested a panel of SSR markers in the attempt to disclose information on the genetic diversity and evolution of the bacterial population, even if, given the reduced spatial and temporal scales of this recent epidemic, a relatively low level of variation was expected. Five SSR markers selected among those previously reported in the literature proved to be polymorphic for the ST53-isolates from Apulia, that even if yielding a small number of alleles (from 2 to 5), when combined provide a good resolution, distinguishing several genotypes. Additionally, the design of a new set of 12 SSR markers for fine-scale genotyping of the Apulian isolates, yielded higher number of allelic variation, paving the way to perform micro-evolutionary and epidemiological studies. Indeed, the successful use of these markers on DNA plant samples, will allow a large-scale study, taking advantage of a six-year dataset of plant DNA collected and stored in the framework of the official monitoring programme started in the region at the beginning of the epidemics in 2013 and covering the entire demarcated area in Apulia that currently exceeds 200,000 ha.

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Xylella fastidiosa: what are the factors that make this bacterium pathogenic and host-specific?

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